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RAW SEQUENCE LISTING

DATE: 07/26/2004

PATENT APPLICATION: US/10/810,262

TIME: 14:42:58

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3 <110> APPLICANT: NAYLOR, STUART
 4 KINGSMAN, SUSAN MARY
 5 BINLEY, KATIE
 7 <120> TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF
 9 <130> FILE REFERENCE: 674523-2029.1
 11 <140> CURRENT APPLICATION NUMBER: 10/810,262
 12 <141> CURRENT FILING DATE: 2004-03-26
 14 <150> PRIOR APPLICATION NUMBER: 09/787,562
 15 <151> PRIOR FILING DATE: 2001-07-06
 17 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03181
 18 <151> PRIOR FILING DATE: 1999-09-22
 20 <150> PRIOR APPLICATION NUMBER: PCT/GB98/02885
 21 <151> PRIOR FILING DATE: 1998-09-23
 23 <150> PRIOR APPLICATION NUMBER: GB 9901906.9
 24 <151> PRIOR FILING DATE: 1999-01-28
 26 <150> PRIOR APPLICATION NUMBER: GB 9903538.8
 27 <151> PRIOR FILING DATE: 1999-02-16
 29 <160> NUMBER OF SEQ ID NOS: 34
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 34 <211> LENGTH: 25
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 44 <212> TYPE: DNA
 45 <213> ORGANISM: Mus sp.
 47 <400> SEQUENCE: 2
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 53 <212> TYPE: DNA
 54 <213> ORGANISM: Artificial Sequence
 56 <220> FEATURE:
 57 <223> OTHER INFORMATION: Description of Artificial Sequence: OBhrel
 58 oligonucleotide
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 63 ccatagtcce gcccttaact ccgcccatac cggccctaac tccgcccagt tccgcccatt 180
 64 ctccgcccga tcgtgacta atttttttta tttatgcaga ggccgaggcc gctcggcct 240

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79 gtcgtgcagg acgtgacatc tagagaacca tcagatgttt ccagggtgcc ccaaggacct 120
80 gaaatgaccc tgtgccttat ttgaactaac caatcagttc gcttctcgct tctgttcgog 180
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89 <220> FEATURE:
90 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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95 acgtcctgca cgactctaga gaaccatcag atgtttccag ggtgccccaa ggacctgaaa 120
96 tgaccctgtg ccttatttga actaaccaat cagttcgctt ctgccttctg ttcgcgcgct 180
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108 gccctgaaca gcccctgag cggcggtcatg cgcggcatca ggggcgctga cttccagtgc 180
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113 tggccccaga agagcgtgtg gcacggctcc gaccccaacg gccgcaggct gaccgagagc 480
114 tactgcgaga cctggcgcac cgaggccccc agcgccaccg ggcaggccag ctccctgctg 540
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125 <221> NAME/KEY: CDS
126 <222> LOCATION: (1)..(633)
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133 gca gtc ttc gtt tgc ccc agc ggt acc gga tcc cac agc cac cgc gac 96
134 Ala Val Phe Val Ser Pro Ser Gly Thr Gly Ser His Ser His Arg Asp
135 20 25 30
137 ttc cag ccg gtg ctc cac ctg gtt gcg ctc aac agc ccc ctg tca ggc 144
138 Phe Gln Pro Val Leu His Leu Val Ala Leu Asn Ser Pro Leu Ser Gly
139 35 40 45
141 ggc atg cgg ggc atc cgc ggg gcc gac ttc cag tgc ttc cag cag gcg 192
142 Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln Cys Phe Gln Gln Ala
143 50 55 60
145 cgg gcc gtg ggg ctg gcg ggc acc ttc cgc gcc ttc ctg tcc tgc cgc 240
146 Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala Phe Leu Ser Ser Arg
147 65 70 75 80
149 ctg cag gac ctg tac agc atc gtg cgc cgt gcc gac cgc gca gcc gtg 288
150 Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala Asp Arg Ala Ala Val
151 85 90 95
153 ccc atc gtc aac ctc aag gac gag ctg ctg ttt ccc agc tgg gag gct 336
154 Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe Pro Ser Trp Glu Ala
155 100 105 110
157 ctg ttc tca ggc tct gag ggt ccg ctg aag ccc ggg gca cgc atc ttc 384
158 Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro Gly Ala Arg Ile Phe
159 115 120 125
161 tcc ttt gac ggc aag gac gtc ctg agg cac ccc acc tgg ccc cag aag 432
162 Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro Thr Trp Pro Gln Lys
163 130 135 140
165 agc gtg tgg cat ggc tgc gac ccc aac ggg cgc agg ctg acc gag agc 480
166 Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg Arg Leu Thr Glu Ser
167 145 150 155 160
169 tac tgt gag acg tgg cgg acg gag gct ccc tgc gcc acg ggc cag gcc 528
170 Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro Ser Ala Thr Gly Gln Ala
171 165 170 175
173 tcc tgc ctg ctg ggg ggc agg ctc ctg ggg cag agt gcc gcg agc tgc 576
174 Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly Gln Ser Ala Ala Ser Cys
175 180 185 190
177 cat cac gcc tac atc gtg ctc tgc att gag aac agc ttc atg act gcc 624
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181 tcc aag tag 633
182 Ser Lys
183 210
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187 <211> LENGTH: 210
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 8
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195 Ala Val Phe Val Ser Pro Ser Gly Thr Gly Ser His Ser His Arg Asp
196           20           25           30
198 Phe Gln Pro Val Leu His Leu Val Ala Leu Asn Ser Pro Leu Ser Gly
199           35           40           45
201 Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln Cys Phe Gln Gln Ala
202           50           55           60
204 Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala Phe Leu Ser Ser Arg
205           65           70           75           80
207 Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala Asp Arg Ala Ala Val
208           85           90           95
210 Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe Pro Ser Trp Glu Ala
211           100          105          110
213 Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro Gly Ala Arg Ile Phe
214           115          120          125
216 Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro Thr Trp Pro Gln Lys
217           130          135          140
219 Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg Arg Leu Thr Glu Ser
220          145          150          155          160
222 Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro Ser Ala Thr Gly Gln Ala
223           165          170          175
225 Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly Gln Ser Ala Ala Ser Cys
226           180          185          190
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229           195          200          205
231 Ser Lys
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244 ggcaacggca agaactacag gggcaccatg agcaagacca agaacggcat cacctgccag 180
245 aagtggagca gcaccagccc ccacaggcct cgcttcagcc ccgccacca cccagcgag 240
246 ggcctggagg agaactactg ccgcaacccc gacaacgacc ccagggccc ttggtgctac 300
247 accaccgacc ctgagaagcg ctacgactac tgcgacatcc tggagtgcga ggaagagtgt 360
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250 aacaagaacc tgaagaagaa ctattgtcgc aatcccgacc gcgagctgcg cccctggtgc 540
251 ttcaccaccg atcccaacaa gcgctgggag ctgtgcgaca tccccgctg caccaccccc 600
252 ccaccagca gcggccccac ctaccagtgc ctgaagggca ccggcgagaa ttaccgggc 660
253 aacgtggccg tgaccgtgag cggccacacc tgccagcact ggagcgccca gacccccac 720
254 acccacaacc gcacccccga gaacttcccc tgcaagaacc tcgacgagaa ttattgccgg 780
255 aacctgacg gcaagagggc cccctggtgc cacaccacca acagccaggt gcgctgggag 840
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261 <211> LENGTH: 912

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272 1 5 10 15
274 gca gtc ttc gtt tcg ccc agc ggt acc gga tcc tta ttt gaa aag aaa 96
275 Ala Val Phe Val Ser Pro Ser Gly Thr Gly Ser Leu Phe Glu Lys Lys
276 20 25 30
278 gtg tat ctc tca gag tgc aag act ggg aat gga aag aac tac aga ggg 144
279 Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly
280 35 40 45
282 acg atg tcc aaa aca aaa aat ggc atc acc tgt caa aaa tgg agt tcc 192
283 Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser Ser
284 50 55 60
286 act tct ccc cac aga cct aga ttc tca cct gct aca cac ccc tca gag 240
287 Thr Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser Glu
288 65 70 75 80
290 gga ctg gag gag aac tac tgc agg aat cca gac aac gat ccg cag ggg 288
291 Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln Gly
292 85 90 95
294 ccc tgg tgc tat act act gat cca gaa aag aga tat gac tac tgc gac 336
295 Pro Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys Asp
296 100 105 110
298 att ctt gag tgt gaa gag gaa tgt atg cat tgc agt gga gaa aac tat 384
299 Ile Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn Tyr
300 115 120 125
302 gac ggc aaa att tcc aag acc atg tct gga ctg gaa tgc cag gcc tgg 432
303 Asp Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala Trp
304 130 135 140
306 gac tct cag agc cca cac gct cat gga tac att cct tcc aaa ttt cca 480
307 Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe Pro
308 145 150 155 160
310 aac aag aac ctg aag aag aat tac tgt cgt aac ccc gat agg gag ctg 528
311 Asn Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu Leu
312 165 170 175
314 cgg cct tgg tgt ttc acc acc gac ccc aac aag cgc tgg gaa ctt tgc 576
315 Arg Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu Cys
316 180 185 190
318 gac atc ccc cgc tgc aca aca cct cca cca tct tct ggt ccc acc tac 624
319 Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr Tyr
320 195 200 205
322 cag tgt ctg aag gga aca ggt gaa aac tat cgc ggg aat gtg gct gtt 672
323 Gln Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala Val
324 210 215 220
326 acc gtg tcc ggg cac acc tgt cag cac tgg agt gca cag acc cct cac 720

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VERIFICATION SUMMARY

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